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| APPLICATION NO. | FILING DATE | FIRST NAMED INVENTOR | ATTORNEY DOCKET NO. | CONFIRMATION NO. |
|---|---|---|---|---|
| 09/601,168 | 07/28/2000 | RICHARD BENAROUS | 935.38812X00 | 8585 |

20457 7590 04/18/2003

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| EXAMINER | |
|---|---|
| SCHNIZER, HOLLY G | |
| ART UNIT | PAPER NUMBER |
| 1653 | 12 |

DATE MAILED: 04/18/2003

Please find below and/or attached an Office communication concerning this application or proceeding.

FILE COPY

| Office Action Summary | Application No. 09/601,168 | Applicant(s) BENAROUS ET AL. | |
|---|---|---|---|
| | Examiner Holly Schnizer | Art Unit 1653 | |

*-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --*

**Period for Reply**

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133).
- Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

**Status**

1)☒ Responsive to communication(s) filed on *15 January 2003* .

2a)☒ This action is **FINAL**. 2b)☐ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

**Disposition of Claims**

4)☒ Claim(s) *1,3,4,6,7 and 22-50* is/are pending in the application.

4a) Of the above claim(s) *6,22-30,33-36 and 38-50* is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *1,3,4,7,31,32 and 37* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

**Application Papers**

9)☐ The specification is objected to by the Examiner.

10)☒ The drawing(s) filed on *29 January 1999* is/are: a)☒ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

11)☐ The proposed drawing correction filed on _____ is: a)☐ approved b)☐ disapproved by the Examiner.

If approved, corrected drawings are required in reply to this Office action.

12)☐ The oath or declaration is objected to by the Examiner.

**Priority under 35 U.S.C. §§ 119 and 120**

13)☒ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☒ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____ .

3.☒ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

14)☐ Acknowledgment is made of a claim for domestic priority under 35 U.S.C. § 119(e) (to a provisional application).

a) ☐ The translation of the foreign language provisional application has been received.

15)☐ Acknowledgment is made of a claim for domestic priority under 35 U.S.C. §§ 120 and/or 121.

**Attachment(s)**

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☐ Information Disclosure Statement(s) (PTO-1449) Paper No(s) _____ .
4) ☐ Interview Summary (PTO-413) Paper No(s). _____ .
5) ☐ Notice of Informal Patent Application (PTO-152)
6) ☐ Other: .

## DETAILED ACTION

### *Status of the Claims*

The Amendment filed January 15, 2003 has been entered and considered. Claims 2 and 5 have been cancelled. Therefore, Claims 1, 3-4, 6-7, and 22-50 are pending. Claims 6, 22-26, 27-30, 33-36, and 38-50 are withdrawn from consideration as being drawn to a non-elected invention. Claims 1, 3-4, 7, 31, 32, and 37 will be considered in this Office Action.

## Objections/Rejections Withdrawn

### *Objection to Specification Withdrawn*

The objection to the Specification for recitation of amino acid sequences without reference to a sequence identifier is withdrawn in light of the amendment.

### *Claim Objections Withdrawn*

The objection to Claim 1 is withdrawn in light of the amendment.

The objection of Claims 7, 31, and 32 because they encompass polynucleotides encoding peptides devoid of the F box and peptides devoid of WD units and therefore encompass non-elected subject matter is withdrawn in light of the amendment to Claim 7. Correction is required.

### *Rejections Withdrawn*

The rejections of Claims 2 and 5 under 35 U.S.C. 112, second paragraph are withdrawn in light of the cancellation of these claims.

The rejection of Claim 27 under 35 U.S.C. 112, second paragraph is withdrawn in light of the amendment making it a non-elected claim.

The rejection of Claim 37 under 35 U.S.C. 112, second paragraph is withdrawn in light of the amendment.

The rejection of Claims 7, 27, 31, 32, and 37 under 35 U.S.C. 112, first paragraph for lack of enablement is withdrawn in light of the amendment removing limitations relating to fragments from the claims.

The rejections of Claims 7, 31, and 32 are rejected under 35 U.S.C. 102(a) and (b) as being anticipated by Skowyra et al. ,Bour et al., Rubinfeld et al., and Inoue et al. is withdrawn in light of the amendment. Skowyra et al., Bour et al., Rubinfeld et al. and Inoue et al. do not teach or suggest that the proteins taught therein contain 7 WD units as found in SEQ ID NO:2 of the present invention.

## Objections/Rejections

### *Claim Objections*

As stated in the previous Office Action (with reference to original claim 1) the claims should refer to sequence identifiers as "SEQ ID NO:1" as indicated in 37 C.F.R. 1.821(d) rather than as "SEQ ID No. 1" as is presently claimed in Claim 7. Correction is required.

***Claim Rejections - 35 USC § 112***

The following is a quotation of the second paragraph of 35 U.S.C. 112:

> The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

Claims 1, 3, 4, 7, 31, 32, and 37 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

Claim 1 is rejected because it is unclear as to whether the claimed protein must only comprise "units having the following positions in SEQ ID NO:2", interpreted to mean that the protein has an F box and 7 WD units, or whether the claimed protein must comprise the sequences having the following positions in SEQ ID NO:2, which would be interpreted to mean that the protein would have to have those identical sequences. Therefore, the metes and bounds of the claim are unclear. Claims 3, 4, 7, 31, 32, and 37 are also rejected since they depend from Claim 1 but do not correct its deficiencies. Clarification is required.

Steps b) and c) of Claim 7 are unclear. First, the claim is drawn to a nucleic acid sequence coding for the h-βTrCP protein consisting of "b) a DNA sequence which hybridizes under strict conditions with the above sequence" (the above sequence is SEQ ID NO:1 which encodes the h-βTrCP protein). This is confusing since a sequence which hybridizes to SEQ ID NO:1 would be complementary to SEQ ID NO:1 and therefore could not encode the h-βTrCP. Second, step c) recites that the DNA

sequence "results from the sequences a) and b) above and codes for the human protein h-βTrCP". However, sequence a) is the sequence of SEQ ID NO:1 and sequence b) is a sequence which hybridizes to SEQ ID NO:1. Thus, sequences a) and b) are complimentary. The claim is unclear as to what type of sequence "results from" two sequences that are complimentary to each other. Third, it is unclear as to what type of sequence "results from the sequence" of b) and codes for the human protein h-βTrCP since these two sequences are complimentary. Claims 31 and 32 are also rejected since they depend from Claim 7 and do not correct its deficiencies. Correction is required.

The following is a quotation of the first paragraph of 35 U.S.C. 112:

> The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

Claims 1, 3, 4, 7, 31, and 32 are rejected under 35 U.S.C. 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention. Applicant is referred to the interim guidelines on written Guidelines published January 5, 2001 in the Federal Register, Vol. 66, No. 4, p. 1099-1111 (available at www.uspto.gov) and the Examiner training Materials on Written Description also available at www.uspto.gov.

The addition of Claims 1, 3, and 4 to this rejection is necessitated by amendment:

Claim 1 has been amended to delete the limitation that the protein has the sequence of SEQ ID NO:2 and to add the limitations previously found in Claim 5. Claim 5 was indicated as allowable because it depended from Claim 1 and thus was drawn to a protein having the sequence of SEQ ID NO:2. However, as amended, the claim is no longer limited to the sequence of SEQ ID NO:2 but may have any number of a wide variety of sequences. Claims 3 and 4 depend from Claim 1 and do not further narrow the genus of sequences claimed.

Applicants contend that the amendment to the claims deleting the limitations relating to peptide fragments is sufficient to overcome the rejection. However, the claims are still drawn to a large genus of protein and nucleic acid sequences as discussed below.

The claims, as amended, are considered to be drawn to any protein or nucleic acid sequence that codes for a protein having the activity of interacting with the Vpu protein of HIV-1, the cell protein IκB, the cell protein β-catenin, or the skp1p protein and having an F-box and seven WD units. The specification discloses a single β-TrCP protein of SEQ ID NO:2 and various modifications of SEQ ID NO:2 wherein a single domain is removed (i.e. SEQ ID NO:2 without an F-box or SEQ ID NO:2 without the first WD domain). The specification and claims do not provide any guidance with respect to the relationship between specific amino acids within the sequence and function. For example, there is no guidance as to what effect changing amino acids within the F-box would have on skp1p binding. The Specification indicates that such changes could affect the binding. For example, page 2 of the Specification states "it is not certain that

the function of the homologous proteins will be totally conserved. Moreover, there are numerous examples which show that there are always significant differences between species" (p. 2, lines 4-6). Thus, the Specification acknowledges that even two highly homologous proteins may not have identical function. However, the Specification does not teach what identifying characteristics of the sequence of the protein of the present invention give it its identifying function. The written description requirement may be satisfied through disclosure of function and minimal structure when there is a well-established correlation between structure and function. In contrast, without such a correlation, the capability to recognize or understand the structure from the mere recitation of function and minimal structure is highly unlikely and is little more than a wish for possession (see Fed. Reg. (2001) Vol. 66(4) p. 1110, Col. 2, citation 49 citing Eli Lilly, 43 USPQ2d at 1406)).

In addition, the specification and claims do not provide any structural or functional characteristics to distinguish a human β-TrCP from that of other species or proteins that have different functions. For example, Hatakeyama et al. (Proc. Natl. Acad. Sci. (1999) 96: 3859-3863), Skowyra et al. (Cell (1997) 91: 209-219) disclose proteins that appear to have the function of the protein of the claimed invention (clm7), that of binding skp1p. The specification does not provide guidance as to whether these proteins of similar function and structure to that of the protein of the present invention are considered modified β-TrCP proteins. Similarly, the specification acknowledges that the previously identified slimb protein and β-TrCP of Xenope are homologs of the protein of the present invention (p.1 lines 19-35). In fact, as shown in Spevak et al.

(Mol. Cell Biol. (1993) 13: 4953-4966), Xenopus β-TrCP has an Fbox and seven WD units that are identical to those of SEQ ID NO:2 (as defined in Claim 1) except for a single amino acid difference in the F-box and a single amino acid difference in the second WD unit. However, the specification does not provide any guidance as to what effect changing a single amino acid in the F-box or WD units would have on activity or the effect that modifications outside the F-box and WD units would have on activity. Moreover, the specification does not provide any structural or functional characteristics of a "human" β-TrCP protein so as to distinguish it from homologs from other species.

Therefore, the scope of the claims include innumerable structural variants (nucleic acid sequences that hybridize and proteins of varying sequences that have an Fbox and seven WD domains) and the genus is highly variant because a significant number of structural differences between genus members is permitted. There is no description of mutational sites that exist in nature, and there is no description of how the structure of the specific SEQ ID NO: relates to the function of the protein or disease. Thus, the common attributes of the genus are not described. One of skill in the art would conclude that applicant was not in possession of the claimed genus because a description of only one member of such a large genus is not representative of the variants of the genus and is insufficient to support the claims.

***Claim Rejections - 35 USC § 102***

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

A person shall be entitled to a patent unless –

(b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

Claims 1, 3, 4, 7, 31, and 32 are rejected under 35 U.S.C. 102(b) as being anticipated by Spevak et al. (Mol. Cell Biol. (1993) 13: 4953-4966).

Spevak et al. disclose a protein that has the units, an F-box and 7 WD domains, as described in present Claim 1. The sequences of the 1st and 3rd –7th WD units of the protein of Spevak et al. are identical to the corresponding sequences in SEQ ID NO:2 (see figure 9, p. 4960 and sequence alignment attached to this Office Action, claimed positions highlighted). The F-Box and 2nd WD unit each have only one amino acid different than the corresponding units of SEQ ID NO:2 (see attached sequence alignment). Thus, the protein of Spevak et al. is considered to comprise the units having the positions in SEQ ID NO:2 described in Claims 1, 3 and 4. The function of a protein (in this case capability of interacting with proteins degradable by proteasome (clm 1), specifically Vpu, IκB or β-catenin (clm 3) or skp1p (clm 4)) is a dependent on its sequence. Two proteins of the same sequence will have the same structure and thus the same function. Thus, since the protein of Spevak et al. has the same sequence and structure as that of the claimed protein, it is an inherent property of the protein described in Spevak et al. that it would have the same function. Thus, claims 1, 3 and 4 are anticipated by Spevak et al.

The DNA sequence encoding the protein disclosed in Spevak et al. is highly homologous to SEQ ID NO:1 (82% local similarity; see sequence alignment attached)

and would hybridize to a polynucleotide having SEQ ID NO:1. Spevak et al. teach that the βTrCP was expressed in cdc20 cells using an expression vector containing the nucleic acid molecule encoding β-TrCP and means for expression, and therefore Spevak et al. meet the limitations of Claims 1, 7, 31, and 32.

It is noted that Claim 1 is unclear as to whether the claimed protein must only comprise "units having the following positions in SEQ ID NO:2", interpreted to mean that the protein has an F box and 7 WD units, or whether the claimed protein must comprise the sequences having the following positions in SEQ ID NO:2, which would be interpreted to mean that the protein would have to have those identical sequences. If the latter is intended then amendment to clarify this intention would overcome the above rejection under 35 U.S.C. 102(b) since the protein of Spevak et al. has a single amino acid difference from that of SEQ ID NO:2 in each of the F-box and 1$^{st}$ WD unit.

***Conclusions***

No Claims are allowable. A thorough search of the prior art did not reveal any teaching or suggestions of a protein having the sequence of SEQ ID NO:2, a nucleic acid molecule encoding the protein of SEQ ID NO: 2 or a nucleic acid molecule having the sequence of SEQ ID NO:1, or a method of identifying anti-HIV-1 antiviral agents using a protein having the sequence of SEQ ID NO:2.

Applicant's amendment necessitated the new ground(s) of rejection presented in this Office action. Accordingly, **THIS ACTION IS MADE FINAL**. See MPEP § 706.07(a). Applicant is reminded of the extension of time policy as set forth in 37 CFR 1.136(a).

A shortened statutory period for reply to this final action is set to expire THREE MONTHS from the mailing date of this action. In the event a first reply is filed within TWO MONTHS of the mailing date of this final action and the advisory action is not mailed until after the end of the THREE-MONTH shortened statutory period, then the shortened statutory period will expire on the date the advisory action is mailed, and any extension fee pursuant to 37 CFR 1.136(a) will be calculated from the mailing date of the advisory action. In no event, however, will the statutory period for reply expire later than SIX MONTHS from the date of this final action.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Holly Schnizer whose telephone number is (703) 305-3722. The examiner can normally be reached on Monday through Wednesday from 8 am to 5:30 pm.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Christopher Low can be reached on (703) 308-2923. The fax phone numbers for the organization where this application or proceeding is assigned are (703) 308-4242 for regular communications and (703) 308-4242 for After Final communications.

Any inquiry of a general nature or relating to the status of this application or proceeding should be directed to the receptionist whose telephone number is (703 308-0196.

Holly Schnizer
April 16, 2003

CHRISTOPHER S. F. LOW
SUPERVISORY PATENT EXAMINER
TECHNOLOGY CENTER 1600

GenCore version 5.1.3


OM protein - protein search, using sw model

Run on: February 20, 2003, 09:55:06 ; Search time 22 Seconds
(without alignments)
2486.386 Million cell updates/sec

Title: US-09-601-168B-2
Perfect score: 3034
Sequence: 1 MDPAEAVLQEKALKFMNSSE.....PAAQAEPPRSPSRTYTYISR 569

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 2597 | 85.6 | 518 | 2 | B48088 | beta-transducin re |
| 2 | 1635.5 | 53.9 | 701 | 2 | T16607 | hypothetical prote |
| 3 | 690 | 22.7 | 506 | 2 | T50211 | WD-repeat protein |
| 4 | 590.5 | 19.5 | 605 | 2 | T38932 | probable sulfur me |
| 5 | 545 | 18.0 | 640 | 2 | S49932 | MET30 protein - ye |
| 6 | 531.5 | 17.5 | 650 | 2 | T46660 | sulfur controller- |
| 7 | 520 | 17.1 | 579 | 2 | T22703 | hypothetical prote |
| 8 | 519.5 | 17.1 | 267 | 2 | S62507 | hypothetical trp-a |
| 9 | 455.5 | 15.0 | 1356 | 2 | T18521 | beta transducin-li |
| 10 | 453 | 14.9 | 775 | 2 | T45136 | WD repeat protein |
| 11 | 413.5 | 13.6 | 1227 | 2 | AE1810 | WD-40 repeat prote |
| 12 | 399 | 13.2 | 779 | 2 | S56245 | cell division cont |
| 13 | 396.5 | 13.1 | 703 | 2 | T43557 | F-box/WD-repeat pr |
| 14 | 378.5 | 12.5 | 1189 | 2 | AI2493 | WD-repeat protein |
| 15 | 375 | 12.4 | 1747 | 2 | AC1842 | WD-40 repeat prote |
| 16 | 374 | 12.3 | 1526 | 2 | AC2239 | WD-40 repeat prote |
| 17 | 373.5 | 12.3 | 1258 | 2 | AI2155 | WD-repeat protein |
| 18 | 373.5 | 12.3 | 1683 | 2 | AF2071 | WD-40 repeat prote |
| 19 | 361.5 | 11.9 | 677 | 2 | AE1861 | serine/threonine k |
| 20 | 358.5 | 11.8 | 559 | 2 | AB2202 | hypothetical prote |
| 21 | 354 | 11.7 | 409 | 2 | S36113 | LIS-1 protein - hu |
| 22 | 354 | 11.7 | 410 | 2 | S48052 | platelet-activatin |
| 23 | 341 | 11.2 | 515 | 2 | S19487 | hypothetical prote |
| 24 | 339.5 | 11.2 | 777 | 2 | T41075 | hypothetical WD-re |
| 25 | 337 | 11.1 | 1146 | 2 | A55532 | myosin-heavy-chain |
| 26 | 336 | 11.1 | 676 | 2 | AH2195 | hypothetical prote |
| 27 | 334 | 11.0 | 589 | 2 | AG2400 | WD-repeat protein |
| 28 | 333.5 | 11.0 | 1711 | 2 | AD1842 | WD-40 repeat prote |
| 29 | 332.5 | 11.0 | 317 | 2 | T46032 | WD-40 repeat regul |
| 30 | 330 | 10.9 | 333 | 2 | G85034 | probable WD-repeat |
| 31 | 320 | 10.5 | 934 | 2 | AG1889 | WD-40 repeat prote |
| 32 | 318 | 10.5 | 422 | 2 | A56640 | CDC4 repeat unit-c |
| 33 | 313.5 | 10.3 | 376 | 2 | T19266 | hypothetical prote |
| 34 | 312.5 | 10.3 | 714 | 2 | S56893 | hypothetical prote |
| 35 | 312 | 10.3 | 786 | 2 | AG2375 | WD-40 repeat-prote |
| 36 | 312 | 10.3 | 876 | 2 | T51507 | WD40-repeat protei |
| 37 | 307.5 | 10.1 | 1693 | 2 | S76086 | beta transducin-li |
| 38 | 306.5 | 10.1 | 598 | 2 | AE2415 | WD-repeat protein |
| 39 | 306 | 10.1 | 1189 | 2 | AH2154 | WD-repeat protein |
| 40 | 305 | 10.1 | 704 | 2 | S33263 | transcription init |
| 41 | 299.5 | 9.9 | 1194 | 2 | T03818 | apoptotic proteina |
| 42 | 298 | 9.8 | 265 | 2 | AF1890 | WD-repeat protein |
| 43 | 297.5 | 9.8 | 357 | 2 | AI2099 | WD-40 repeat prote |
| 44 | 297 | 9.8 | 502 | 2 | T41148 | trp-asp repeat con |
| 45 | 296.5 | 9.8 | 304 | 2 | AG1837 | WD-40 repeat prote |

ALIGNMENTS

RESULT 1
B48088
beta-transducin repeat-containing protein - African clawed frog
N;Alternate names: beta-Trcp
C;Species: Xenopus laevis (African clawed frog)
C;Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 21-Jul-2000
C;Accession: B48088
R;Spevak, W.; Kelper, B.D.; Stratowa, C.; Castanon, M.J.
Mol. Cell. Biol. 13, 4953-4966, 1993
A;Title: Saccharomyces cerevisiae cdc15 mutants arrested at a late stage in anaphase
A;Reference number: A48088; MUID:93330289; PMID:8393141
A;Accession: B48088
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-518 <SPE>
A;Cross-references: GB:M98268; NID:g295542; PIDN:AAA02810.1; PID:g295543
C;Superfamily: unassigned WD repeat proteins; WD repeat homology
C;Keywords: duplication
F;431-462/Domain: WD repeat homology <WD1>

Query Match 85.6%; Score 2597; DB 2; Length 518;
Best Local Similarity 91.6%; Pred. No. 1.2e-193;
Matches 488; Conservative 7; Mismatches 8; Indels 30; Gaps 1;

```
Qy      18 SSEREDCNNGEPPRKIIPEKNSLRQTYNSCARLCLNQETVCLASTAMKTENCVAKTKLAN 77
           :|||||||  |||||||  |||:|||                                ||||
Db      13 ASEREDCNRDEPPRKIITEKNTLRQ----------------------------TKLAN 42

Qy      78 GTSSMIVPKQRKLSASYEKEKELCVKYFEQWSESDQVEFVEHLISQMCHYQHGHINSYLK 137
           |||||||||||||:|||||||||||||||||| ||||||||||:||||||||||:|||
Db      43 GTSSMIVPKQRKLSANYEKEKELCVKYFEQWSECDQVEFVEHLISRMCHYQHGHINTYLK 102

Qy     138 PMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELVCKEWYRVTSDGMLWKKLIERMV 197
           |||||||||||||||||||||||||||||||||:|||||||||||||||||||||||||
Db     103 PMLQRDFITALPARGLDHIAENILSYLDAKSLCSAELVCKEWYRVTSDGMLWKKLIERMV 162

Qy     198 RTDSLWRGLAERRGWGQYLFKNKPPDGNAPPNSFYRALYPKIIQDIETIESNWRCGRHSL 257
           |||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db     163 RTDSLWRGLAERRGWGQYLFKNKPPDGKTPPNSFYRALYPKIIQDIETIESNWRCGRHSL 222

Qy     258 QRIHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIWDKNTLECKRILVGHTGSVLCLQYDE 317
           |||||||||||||||||||||||||||||||||||||||||||:|||||||||||||||
Db     223 QRIHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIWDKNTLECKRVLMGHTGSVLCLQYDE 282

Qy     318 RVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNGMMVTCSKDRSIAVWDMASP 377
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     283 RVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNGMMVTCSKDRSIAVWDMASA 342

Qy     378 TDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVWNTSTCEFVRTLNGHKRGIACLQ 437
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     343 TDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVWNTSTCEFVRTLNGHKRGIACLQ 402
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Qy    438 YRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEEEVRCIRFDNKRIVSGAYDGKIKVWDL 497
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    403 YRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDL 462

Qy    498 VAALDPRAPAGTLCLRTLVEHSGRVFRLQFDEFQIVSSSHDDTILIWDFLNDP 550
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    463 VAALDPRAPAGTLCLRTLVEHSGRVFRLQFDEFQIVSSSHDDTILIWDFLNDP 515


RESULT 2
T16607
hypothetical protein K10B2.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T16607
R;Miller, N.
submitted to the EMBL Data Library, June 1995
A;Description: The sequence of C. elegans cosmid K10B2.
A;Reference number: Z18545
A;Accession: T16607
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-701 <MIL>
A;Cross-references: EMBL:U28730; NID:g860694; PID:g860695; PIDN:AAA68258.1; CESP:K10B2.1
A;Experimental source: strain Bristol N2
C;Genetics:
A;Gene: CESP:K10B2.1
A;Introns: 78/3; 125/1; 183/2; 281/3; 404/3; 551/3; 668/3

  Query Match             53.9%;  Score 1635.5;  DB 2;  Length 701;
  Best Local Similarity   57.7%;  Pred. No. 8.1e-119;
  Matches  328;  Conservative   69;  Mismatches  116;  Indels   55;  Gaps    8;

Qy     31 RKIIPEKNSLRQTYNSCARLCLNQETVCLASTAMKTENCVAKTKLAN----------GTS 80
          |:    | :|:|   :     :   |||:::     | |   | ::|
Db      2 RRFREGKRALKQRGRARDGGSIQALTVCVST----IERCF--TAVSNPIFFLFSTFFSVF 55

Qy     81 SMIVPKQR-----KLSASYEKEKELCVKYFEQWSESDQVEFVEHLISQMCHYQHGHINSY 135
          | : | :        | |:    |:      :||| :|::|:: :: :: ||| | ::::
Db     56 SFLFPSRNTQIFLSYSRSFSSFSEVL-----KWSEHEQLDFMDKIVHRLSHYQLGKVDNF 110

Qy    136 LKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELVCKEWYRVTSDGMLWKKLIER 195
          ::|||||||: |||    |: | ||  ::: || : | |    |    : |  ||||||:
Db    111 IRPMLQRDFISNLPA----HLVELILFNVNSDSLKSCEEVSTSWRCALARGQHWKKLIEK 166

Qy    196 MVRTDSLWRGLAERRGWGQYL--------------------FKNKPPDGNAPPNSFYRAL 235
          ||:|||| ||:|:| | ::|                    |    |     : ||  |
Db    167 NVRSDSLWWGLSEKRQWDKFLNISRDMSVRRICEKFNYDVNIKRDKLDQLILMHVFYSKL 226

Qy    236 YPKIIQDIETIESNWRCGRHSLQRIHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIWDKN 295
          |||||:||  |::||: | : : ||:|:|| |||||||||| ||||||||||||||:
Db    227 YPKIIRDIHNIDNNWKRGNYKMTRINCQSENSKGVYCLQYDDDKIVSGLRDNTIKIWDRK 286

Qy    296 TLECKRILTGHTGSVLCLQYDERVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRF 355
          | |||:|||||||||||| ||||:||||:||||||| ||| : ||||||||||||||
Db    287 DYSCSRILSGHTGSVLCLQYDNRVIISGSSDATVRVWDVETGECIKTLIHHCEAVLHLRF 346

Qy    356 NNGMMVTCSKDRSIAVWDMASPTDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVW 415
          ||:|||||||||||||| || |||:||||||||||||||||:|||||||||||||||||
Db    347 ANGIMVTCSKDRSIAVWDMVSPRDITIRRVLVGHRAAVNVVDFDDRYIVSASGDRTIKVW 406

Qy    416 NTSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRC 475
          :  | |||||| ||:|||||||||| |||||||||||||||||  | ||||||||||||||
Db    407 SMDTLEFVRTLAGHRRGIACLQYRGRLVVSGSSDNTIRLWDIHSGVCLRVLEGHEELVRC 466

Qy    476 IRFDNKRIVSGAYDGKIKVWDLVAALDPRAPAGTLCLRTLVEHSGRVFRLQFDEFQIVSS 535
          |||| ||||||||||||||||| ||||||| :  :|| :||:|:|||||||||:||||||
Db    467 IRFDEKRIVSGAYDGKIKVWDLQAALDPRALSSEICLCSLVQHTGRVFRLQFDDFQIVSS 526

Qy    536 SHDDTILIWDFLNDPAAQAEPPRSPSRT 563
          |||||||||||: |     |   || |
Db    527 SHDDTILIWDFLDAP-----PSGLPSST 549
```

```
RESULT 3
T50211
WD-repeat protein [imported] - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 02-Sep-2000
C;Accession: T50211
R;McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.; Brown, S.; Murphy, L.; Jones, L.;
submitted to the EMBL Data Library, January 2000
A;Reference number: Z25046
A;Accession: T50211
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-506 <MCD>
A;Cross-references: EMBL:AL136538; PIDN:CAB66464.1; GSPDB:GN00066; SPDB:SPAC30.05
A;Experimental source: strain 972h(-); cosmid c30
C;Genetics:
A;Gene: SPAC29E6.01; SPDB:SPAC30.05
A;Map position: 1
A;Introns: 43/1; 74/3
C;Superfamily: unassigned WD repeat proteins; WD repeat homology

  Query Match             22.7%;  Score 690;  DB 2;  Length 506;
  Best Local Similarity   30.4%;  Pred. No. 1.3e-45;
  Matches  163;  Conservative  104;  Mismatches  167;  Indels  102;  Gaps   15;

Qy     67 ENCVAK----TKLANGTSSMIVPKQRKLSASYEKEKELCVKYFEQWSESDQVEFVEHLIS 122
          :| |:|    |  :: ::|  ||    ||                  |:::::  :  |::
Db      8 KNVVSKVSDLTSCSDFSTSSPVPCLNPLS----------------HENNRIDLIRDLLA 50

Qy    123 QMCHYQHGHINSYLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELVCKEWYRV 182
          :       : :::: :|  ||     |    : ::  : ||||   ||  :|: | | |:
Db     51 SLSKEGVVAVYNHVRSLLFTDFTEVFP----EEVSLRVFSYLDQLDLCKCKLMSKRWKRL 106

Qy    183 TSDGMLWKKLI--------ERMVRTDSLWRG------------LAERRGWG--------- 213
          |  :|| |           | ::     ||             | ::   |
Db    107 LEDPGIWKALYMQKGWFVNENVLNEFEAWRRTHKFPQPRFENFLKQQNIIGPYGTMFLPQ 166

Qy    214 QYLFKNKPPDGNAPPNSFYRALYPKIIQDIETIESNWRCGRHSLQRIHCRS--------- 264
          |::|     | |  |   :  ||    ::   ::|||| ||  :   :  |
Db    167 QFIF-----DSNGRPLLNWSYLY----KEHAHLDSNWRHGRFLVSTFNNPSIRFPADQDF 217

Qy    265 -ETSKGVYCLQYDDQKIVSGLRDNTIKIWDKNTLECKRILTGHTGSVLCLQYDER--VII 321
           |   |||:|||: :||| :| |: :|| |:       | ||:|||||| :  |  :::
Db    218 RATLDSVYCVQYDDEIMVSGSKDRTVSVWDVNSRFILYKLYGHSGSVLCLDFCRRRNLLV 277

Qy    322 TGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNGMMVTCSKDRSIAVW--DMASPTD 379
          :||||||: :||      |  : || :  :   ::: |:| :  ||  |  || :
Db    278 SGSSDSTIIIWDWQNRRPLKVYFGHTDNVLGVVVSENYIISSSRDHTARVWRLDATSPAE 337

Qy    380 ITLRRVLVGHRAAVNVVDFDDK--YIVSASGDRTIKVWNTSTCEFVRTLNGHKRGIACLQ 437
          :  || || |:|| | :  |   ||:|| |||:: |: :|   :| :: |:|||| |
Db    338 ACM-HVLRGHLASVNSVQYSSKTGLIVTASSDRTLRTWDITTGHCIRIIHAHQRGIACAQ 396

Qy    438 YRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDL 497
          |  : :|||||| |||:::   |  ||:|:|||:|:| :|||:::|||| ||| :::|:
Db    397 YNGKFIVSGSSDLTIRIFEASSGKLLRMLQGHEDLIRTVRFNDEKIVSGGYDGTVRIWN- 455

Qy    498 VAALDPRAPAGTLCLRTLVEH-------SGRVFRLQFDEFQIVSSSHDDTILIWDF 546
                    |  :|       : ||| ||||  :|:: :|   ||:|:|
Db    456 --------------FNTGEQHCVLHNSRNSRVFGLQFDHRRIIACTHSSEILVWNF 497


RESULT 4
T38932
probable sulfur metabolite control protein - fission yeast (Schizosaccharomyces pombe
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 26-May-2000
C;Accession: T38932
R;Badcock, K.; Churcher, C.M.; Wood, V.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, April 1997
A;Reference number: Z21818
A;Accession: T38932
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nucleic - nucleic search, using sw model

February 21, 2003, 21:18:21 ; Search time 5545 Seconds
(without alignments)
11289.474 Million cell updates/sec

Title: US-09-601-168B-1
Perfect score: 2151
Sequence: 1 tgcgttggctgcggcctggc.....gttttgccagaaaaaaaaaa 2151

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 2151 | 100.0 | 2151 | 6 | AX019507 | AX019507 Sequence |
| 2 | 2151 | 100.0 | 2151 | 6 | AX057166 | AX057166 Sequence |
| 3 | 2151 | 100.0 | 2151 | 9 | AF129530 | AF129530 Homo sapi |
| 4 | 2151 | 100.0 | 2151 | 9 | HSBTRCP | Y14153 Homo sapien |
| 5 | 2030.4 | 94.4 | 2308 | 9 | BC027994 | BC027994 Homo sapi |
| 6 | 1682.2 | 78.2 | 2175 | 10 | AF081887 | AF081887 Mus muscu |
| 7 | 1663.2 | 77.3 | 1818 | 9 | AF101784 | AF101784 Homo sapi |
| 8 | 1630.4 | 75.8 | 2081 | 10 | BC003989 | BC003989 Mus muscu |
| 9 | 1567.2 | 72.9 | 1979 | 10 | AF110396 | AF110396 Mus muscu |
| 10 | 1451.2 | 67.5 | 1712 | 10 | AF099932 | AF099932 Mus muscu |
| 11 | 1442.8 | 67.1 | 1710 | 10 | AF112979 | AF112979 Mus muscu |
| 12 | 1017.8 | 47.3 | 1671 | 5 | XELSBTRCP | M98268 African cla |
| 13 | 883.4 | 41.1 | 2134 | 9 | AB033279 | AB033279 Homo sapi |
| 14 | 883.4 | 41.1 | 2252 | 9 | AB033280 | AB033280 Homo sapi |
| 15 | 883.4 | 41.1 | 2274 | 9 | AB033281 | AB033281 Homo sapi |
| 16 | 883.4 | 41.1 | 4230 | 9 | AB014596 | AB014596 Homo sapi |
| 17 | 883.4 | 41.1 | 4395 | 9 | BC026213 | BC026213 Homo sapi |
| 18 | 882.4 | 41.0 | 1653 | 9 | AF176022 | AF176022 Homo sapi |
| 19 | 877.8 | 40.8 | 4030 | 10 | BC034261 | BC034261 Mus muscu |
| 20 | 853.2 | 39.7 | 1970 | 10 | AY038079 | AY038079 Mus muscu |
| c 21 | 757.8 | 35.2 | 67008 | 9 | AP000252 | AP000252 Homo sapi |
| c 22 | 757.8 | 35.2 | 100000 | 9 | AP000212 | AP000212 Homo sapi |
| c 23 | 757.8 | 35.2 | 100000 | 17 | AP000134 | Ap000134 Homo sapi |
| c 24 | 757.8 | 35.2 | 149298 | 9 | AP000031 | AP000031 Homo sapi |
| c 25 | 757.8 | 35.2 | 340000 | 9 | AP001711 | AP001711 Homo sapi |
| 26 | 676.4 | 31.4 | 2534 | 3 | AY118898 | AY118898 Drosophil |
| 27 | 673.2 | 31.3 | 2154 | 3 | AF032878 | AF032878 Drosophil |
| 28 | 673.2 | 31.3 | 2367 | 3 | AF222924 | AF222924 Drosophil |
| 29 | 673.2 | 31.3 | 3532 | 3 | AF222923 | AF222923 Drosophil |
| 30 | 583.2 | 27.1 | 188524 | 2 | AC112602 | AC112602 Rattus no |
| 31 | 518.8 | 24.1 | 1561 | 6 | AX057148 | AX057148 Sequence |
| 32 | 512 | 23.8 | 934 | 5 | XLU63921 | U63921 Xenopus lae |
| 33 | 502.6 | 23.4 | 1827 | 5 | XLU63922 | U63922 Xenopus lae |
| 34 | 463.6 | 21.6 | 2983 | 10 | BC008552 | BC008552 Mus muscu |
| 35 | 454 | 21.1 | 1443 | 3 | AF339101 | AF339101 Heteroder |
| 36 | 453.2 | 21.1 | 2700 | 3 | AF275253 | AF275253 Caenorhab |
| 37 | 333.2 | 15.5 | 108503 | 9 | AL627424 | AL627424 Human DNA |
| c 38 | 288 | 13.4 | 173634 | 3 | AC009344 | AC009344 Drosophil |
| c 39 | 288 | 13.4 | 230266 | 3 | AE003733 | AE003733 Drosophil |
| c 40 | 277.2 | 12.9 | 40472 | 2 | AC014085 | AC014085 Drosophil |
| 41 | 252.8 | 11.8 | 17344 | 3 | U28730 | U28730 Caenorhabdi |
| 42 | 232.8 | 10.8 | 143078 | 9 | AL445463 | AL445463 Human DNA |
| 43 | 225.4 | 10.5 | 231703 | 2 | AC126454 | AC126454 Mus muscu |
| 44 | 225 | 10.5 | 266 | 10 | F391178S09 | AF391186 Mus muscu |
| c 45 | 216.2 | 10.1 | 261252 | 2 | AC111315 | AC111315 Rattus no |

ALIGNMENTS

RESULT 1
AX019507
LOCUS AX019507 2151 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 1 from Patent WO9938969.
ACCESSION AX019507
VERSION AX019507.1 GI:10043427
KEYWORDS .
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 2151)
AUTHORS Arenzana,S.F., Concordet,J.P., Kroll,M., Durand,H., Benarous,R. and Margottin,F.
TITLE Protein humaine beta -trcp
JOURNAL Patent: WO 9938969-A 1 05-AUG-1999;

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Db    1141 ACCCTCAGGAGGGTGCTGGTGGGACACCGAGCTGCGGTCAATGTTGTAGACTTTGATGAC 1200

Qy    1270 AAGTACATTGTTTCTGCATCTGGGGATAGAACTATAAAGGTATGGAACACAAGTACTTGT 1329
           ||||||| |||||||| ||||| |||||||| |||||||| ||||||||||||| |||
Db    1201 AAGTACATCGTTTCTGCCTCTGGAGATAGAACCATAAAGGTGTGGAACACAAGTACCTGT 1260

Qy    1330 GAATTTGTAAGGACCTTAAATGGACACAAACGAGGCATTGCCTGTTTGCAGTACAGGGAC 1389
           ||||| ||||||||| ||||||| ||||| || ||||| |||||||||||||||| |||
Db    1261 GAATTCGTAAGGACCCTAAATGGGCACAAGCGTGGCATCGCCTGTTTGCAGTACAGAGAC 1320

Qy    1390 AGGCTGGTAGTGAGTGGCTCATCTGACAACACTATCAGATTATGGGACATAGAATGTGGT 1449
           |||||||| ||||| ||||| |||||||||| ||||| | |||||||||| |||||
Db    1321 AGGCTGGTGGTGAGCGGCTCCTCTGACAACACCATCAGGCTGTGGGACATAGAGTGTGGA 1380

Qy    1450 GCATGTTTACGAGTGTTAGAAGGCCATGAGGAATTGGTGCGTTGTATTCGATTTGATAAC 1509
           |||||  | |||||||| || |||||||||| ||||| || || ||||||||||||||
Db    1381 GCATGCCTGCGAGTGTTGGAGGGCCATGAGGAGTTGGTACGCTGCATTCGATTTGATAAC 1440

Qy    1510 AAGAGGATAGTCAGTGGGGCCTATGATGGAAAAATTAAAGTGTGGGATCTTGTGGCTGCT 1569
           || |||||||| || || |||||||||| |||||||||||||||||||| ||||||||
Db    1441 AAAAGGATAGTGAGCGGAGCCTATGATGGGAAAATTAAAGTGTGGGATCTTATGGCTGCT 1500

Qy    1570 TTGGACCCCCGTGCTCCTGCAGGGACACTCTGTCTACGGACCCTTGTGGAGCATTCCGGA 1629
           |||||||| |||||||| ||||||| |||||||| ||||| |||||||||||||| |||
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Qy    1630 AGAGTTTTTCGACTACAGTTTGATGAATTCCAGATTGTCAGTAGTTCACATGATGACACA 1689
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Qy    1750 TCTCGAACATACACCTACATCTCCAGATAA 1779
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Db    1681 TCTCGGACATACACCTACATCTCCAGATAA 1710


RESULT 12
XELSBTRCP
LOCUS       XELSBTRCP              1671 bp    mRNA    linear   VRT 17-SEP-1993
DEFINITION  African clawed frog beta-TrCP mRNA, complete cds.
ACCESSION   M98268
VERSION     M98268.1  GI:295542
KEYWORDS    beta-transducin repeats.
SOURCE      Xenopus laevis (library: S. cerevisiae expression library of
            X.laevis oocytes) cDNA to mRNA.
  ORGANISM  Xenopus laevis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus.
REFERENCE   1  (bases 1 to 1671)
  AUTHORS   Spevak,W., Keiper,B.D., Stratowa,C. and Castanon,M.J.
  TITLE     Saccharomyces cerevisiae cdc15 mutants arrested at a late stage in
            anaphase are rescued by Xenopus cDNAs encoding N-ras or a protein
            with beta-transducin repeats
  JOURNAL   Mol. Cell. Biol. 13 (8), 4953-4966 (1993)
  MEDLINE   93330289
   PUBMED   8393141
FEATURES             Location/Qualifiers
     source          1. .1671
                     /organism="Xenopus laevis"
                     /db_xref="taxon:8355"
                     /cell_type="oocyte"
                     /tissue_lib="S. cerevisiae expression library of X.laevis
                     oocytes"
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                     /gene="beta-TrCP"
                     48. .1604
                     /gene="beta-TrCP"
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                     /protein_id="AAA02810.1"
                     /db_xref="GI:295543"
                     /translation="MEGFSCSLQPPTASEREDCNRDEPPRKIITEKNTLRQTKLANGT
                     SSMIVPKQRKLSANYEKEKELCVKYFEQWSECDQVEFVEHLISRMCHYQHGHINTYLK
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                     RHSLQRIHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIWDKNTLECKRVLMGHTGSVL
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                     AVWDMASATDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVWNTSTCEFVRTLN
                     GHKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVS
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                     /gene="beta-TrCP"
BASE COUNT      495 a    341 c    424 g    411 t
ORIGIN

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  Best Local Similarity  81.8%;  Pred. No. 1e-278;
  Matches 1175;  Conservative    0;  Mismatches  262;  Indels    0;  Gaps    0;

Qy     284 AAACAAAACTTGCCAATGGCACTTCCAGTATGATTGTGCCCAAGCAACGGAAACTCTCAG 343
           | |||||||||||||||||||||||||||||||||||||||||||| || ||||| ||||
Db     157 AGACAAAACTTGCCAATGGCACTTCCAGCATGATTGTGCCCAAGCAGCGAAAACTGTCAG 216

Qy     344 CAAGCTATGAAAAGGAAAAGGAACTGTGTGTCAAATACTTTGAGCAGTGGTCAGAGTCAG 403
           |||  || || |||||||| || || || ||||| || |||||||||||||| ||||  |
Db     217 CAAATTACGAGAAGGAAAAAGAGCTATGCGTCAAGTATTTTGAGCAGTGGTCCGAGTGCG 276

Qy     404 ATCAAGTGGAATTTGTGGAACATCTTATATCCCAAATGTGTCATTACCAACATGGGCACA 463
           ||||||| || ||||| ||||| || ||||| | |||||| || || || ||||| || |
Db     277 ATCAAGTAGAGTTTGTTGAACACCTGATATCTCGAATGTGCCACTATCAGCATGGACATA 336

Qy     464 TAAACTCGTATCTTAAACCTATGTTGCAGAGAGATTTCATAACTGCTCTGCCAGCTCGGG 523
           ||||| | || ||||| || ||||| || || |||||||| || || || |||||||| |
Db     337 TAAACACTTACCTTAAGCCAATGTTACAAAGGGATTTCATTACCGCACTACCAGCTCGCG 396

Qy     524 GATTGGATCATATCGCTGAGAACATTCTGTCATACCTGGATGCCAAATCACTATGTGCTG 583
           || | ||||| || || || || || || |||||||||||||| || ||| | ||| |||
Db     397 GACTCGATCACATAGCAGAAAATATACTTTCATACCTGGATGCAAAGTCATTGTGTTCTG 456

Qy     584 CTGAACTTGTGTGCAAGGAATGGTACCGAGTGACCTCTGATGGCATGCTGTGGAAGAAGC 643
           | ||||| || || ||||| ||||| |||||||||| ||||| ||||| ||||| ||||
Db     457 CAGAACTGGTATGTAAGGAGTGGTATCGAGTGACCTCAGATGGAATGCTCTGGAAAAAGC 516

Qy     644 TTATCGAGAGAATGGTCAGGACAGATTCTCTGTGGAGAGGCCTGGCAGAACGAAGAGGAT 703
           | || ||| | |||||| |||||||||||||| |||||||| |||||||||  ||||||||
Db     517 TCATAGAGCGGATGGTCCGGACAGATTCTCTTTGGAGAGGACTGGCAGAAAGAAGAGGAT 576

Qy     704 GGGGACAGTATTTATTCAAAAACAAACCTCCTGACGGGAATGCTCCTCCCAACTCTTTTT 763
           |||| || ||||| || |||||||||||||| || |||||  | || || || || || | |
Db     577 GGGGGCAATATTTGTTTAAAAACAAACCTCCAGATGGGAAAACGCCACCAAATTCATTCT 636

Qy     764 ATAGAGCACTTTATCCTAAAATTATACAAGACATTGAGACAATAGAATCTAATTGGAGAT 823
           | ||||| ||||| || |||||||| |||||||| |||||||| || || || ||| | |
Db     637 ACAGAGCGCTTTACCCAAAAATTATTCAAGACATAGAGACAATCGAGTCCAACTGGCGCT 696

Qy     824 GTGGAAGACATAGTTTACAGAGAATTCACTGCCGAAGTGAAACAAGCAAAGGAGTTTACT 883
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Qy     884 GTTTACAGTATGATGATCAGAAAATAGTAAGCGGCCTTCGAGACAACACAATCAAGATCT 943
           || | ||||| |||||||||| |||||||| || ||  |||| |||| || |||||||
Db     757 GTCTGCAGTACGATGATCAGAAGATAGTAAGTGGACTCAGAGATAACACCATTAAGATCT 816

Qy     944 GGGATAAAAACACATTGGAATGCAAGCGAATTCTCACAGGCCATACAGGTTCAGTCCTCT 1003
           ||||||| || || ||||| ||||||||| | || |  || || || || ||||| ||||
Db     817 GGGATAAGAATACTTTGGAGTGCAAGCGAGTGCTGATGGGTCACACTGGGTCAGTTCTCT 876

Qy    1004 GTCTCCAGTATGATGAGAGAGTGATCATAACAGGATCATCGGATTCCACGGTCAGAGTGT 1063
           |||| || |||||||||||||| ||||| || || || || || || || ||| | ||||
Db     877 GTCTGCAATATGATGAGAGAGTAATCATTACTGGCTCTTCAGACTCTACCGTCCGGGTGT 936
```

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1630 AGAGTTTTTCGACTACAGTTTGATGAATTCCAGATTGTCAGTAGTTCACATGATGACACA 1689
     |||||||| || || ||||||||||||||||||||||||||||||||||||||||||||||
1561 AGAGTTTTCCGCCTCCAGTTTGATGAATTCCAGATTGTCAGTAGTTCACATGATGACACA 1620

1690 ATCCTCATCTGGGACTTCCTAAATGATCCAGCTGCCCAAGCTGAACCCCCCCCGTTCCCCT 1749
     || |||||||||||||||| |||||||||||||| || |||||||| ||||| ||||||
1621 ATTCTCATCTGGGACTTCCTGAATGATCCAGCTGCTCACGCTGAACCGCCCCGCTCCCCT 1680

1750 TCTCGAACATACACCTACATCTCCAGATAAAT 1781
     ||||| |||||||||||||||||||||||||
1681 TCTCGGACATACACCTACATCTCCAGATAAAT 1712
```

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RESULT 11
AF112979
LOCUS       AF112979               1710 bp    mRNA    linear   ROD 02-MAR-1999
DEFINITION  Mus musculus beta-transducin repeat containing protein mRNA,
            complete cds.
ACCESSION   AF112979
VERSION     AF112979.1  GI:4140717
KEYWORDS    .
SOURCE      Mus musculus.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 1710)
  AUTHORS   Spencer,E., Jiang,J. and Chen,Z.J.
  TITLE     Signal-induced ubiquitination of IkappaBalpha by the F-box protein
            Slimb/beta-TrCP
  JOURNAL   Genes Dev. 13 (3), 284-294 (1999)
  MEDLINE   99145465
   PUBMED   9990853
REFERENCE   2  (bases 1 to 1710)
  AUTHORS   Chen,Z.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-DEC-1998) Molecular Biology and Oncology, UT
            Southwestern Medical Ceter, 5323 Harry Hines Blvd, Dallas, TX
            75235-9148, USA
FEATURES             Location/Qualifiers
     source          1. .1710
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
     CDS             1. .1710
                     /function="ubiquitinates phosphorylated IkBa"
                     /note="beta-TrCP; F-box protein; IkB-ubiquitin ligase;
                     substrate recognition subunit of SCF complex; similar to
                     Homo sapiens beta-TrCP and Drosophila melanogaster Slimb"
                     /codon_start=1
                     /product="beta-transducin repeat containing protein"
                     /protein_id="AAD04181.1"
                     /db_xref="GI:4140718"
                     /translation="MDPAEAVLQEKALKFMNSSEREDCNNGEPPRKIIPEKNSLRQTY
                     NSCARLCINQETVCLTSTAMKTENCVAKAKLANGTSSMIVPKQRKLSASYEKEKELCV
                     KYFEQWSESDQVEFVEHLISQMCHYQHGHINSYLKPMLQRDFITALPARGLDHIAENI
                     LSYLDAKSLCAAELVCKEWYRVTSDGMLWKKLIERMVRTDSLWRGLAERRGWGQYLFK
                     NKPPDENAPPNSFYRALYPKIIQDIETIESNWRCGRHSLQRIHCRSETSKGVYCLQYD
                     DQKIVSGLRDNTIKIWDKSTLECKRILTGHTGSVLCLQYGERVIITGSSDSTVRVWDV
                     NAGEMLNTLIHHCEAVLHLRFNNGMMVTCSKDRSIAVWDMASPTDITLRRVLVGHRAA
                     VNVVDFDDKYIVSASGDRTIKVWNTSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDN
                     TIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLMAALDPRAPAG
                     TLCLRTLVEHSGRVFRLQFDEFQIVSSSHDDTILIWDFLNDPAAHAEPPRSPSRTYTY
                     ISR"
BASE COUNT      469 a    399 c    453 g    389 t
ORIGIN
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  Query Match           67.1%;  Score 1442.8;  DB 10;  Length 1710;
  Best Local Similarity  90.2%;  Pred. No. 0;
  Matches 1543;  Conservative    0;  Mismatches  167;  Indels    0;  Gaps    0;

Qy      70 ATGGACCCGGCCGAGGCGGTGCTGCAAGAGAAGGCACTCAAGTTTATGAATTCCTCAGAG 129
           |||||||||| |||||||||||||| ||||| || || ||||||||||||||||||||||
Db       1 ATGGACCCGGCAGAGGCGGTGCTGCAGGAGAAAGCGCTTAAGTTTATGAATTCCTCAGAG 60

Qy     130 AGAGAAGACTGTAATAATGGCGAACCCCCTAGGAAGATAATACCAGAGAAGAATTCACTT 189
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 AGAGAAGACTGTAATAATGGCGAACCCCCTAGGAAGATAATACCAGAGAAGAATTCACTT 120

Qy     190 AGACAGACATACAACAGCTGTGCCAGACTCTGCTTAAACCAAGAAACAGTATGTTTAGCA 249
           |||||||| |||||||||||||||||| || ||| |||||||||| |||||||||| || ||
Db     121 AGACAGACTTACAACAGCTGTGCCAGGCTTTGCATAAACCAAGAGACAGTATGTCTAACA 180

Qy     250 AGCACTGCTATGAAGACTGAGAATTGTGTGGCCAAAACAAAACTTGCCAATGGCACTTCC 309
           |||||||||||||||||| ||||||||||||||| | ||||||||||||||||||||||
Db     181 AGCACTGCTATGAAGACTGAAAATTGTGTGGCCAAAGCCAAACTTGCCAATGGCACTTCC 240

Qy     310 AGTATGATTGTGCCCAAGCAACGGAAACTCTCAGCAAGCTATGAAAAGGAAAAGGAACTG 369
           || |||||||||||||||| |||||||||||||||||||||||| |||||||||| ||| |
Db     241 AGCATGATTGTGCCCAAGCAGCGGAAACTCTCAGCAAGCTATGAGAAGGAAAAGGAGCTG 300

Qy     370 TGTGTCAAATACTTTGAGCAGTGGTCAGAGTCAGATCAAGTGGAATTTGTGGAACATCTT 429
           |||||||| || |||||||||||||||||||||||||||||||||||||| ||||| |||
Db     301 TGTGTCAAGTATTTTGAGCAGTGGTCAGAGTCTGATCAAGTGGAATTTGTAGAACACCTT 360

Qy     430 ATATCCCAAATGTGTCATTACCAACATGGGCACATAAACTCGTATCTTAAACCTATGTTG 489
           |||||||||||||||| ||||| |||||||||| ||||| || || ||||||||| ||
Db     361 ATATCCCAAATGTGTCACTACCAGCATGGGCACATCAACTCCTACCTAAAACCTATGCTG 420

Qy     490 CAGAGAGATTTCATAACTGCTCTGCCAGCTCGGGGATTGGATCATATCGCTGAGAACATT 549
           ||||| |||||||||||||| |||||||| |||||  |||| || ||||||||||||||||
Db     421 CAGAGGGATTTCATAACTGCACTGCCAGCACGGGGTCTGGACCACATCGCTGAGAACATT 480

Qy     550 CTGTCATACCTGGATGCCAAATCACTATGTGCTGCTGAACTTGTGTGCAAGGAATGGTAC 609
           ||||||||| |||| ||||| ||||| |||||||||||| || ||||||||||||||||||
Db     481 CTGTCATACTTGGACGCCAAGTCACTGTGTGCTGCTGAGCTCGTGTGCAAGGAATGGTAC 540

Qy     610 CGAGTGACCTCTGATGGCATGCTGTGGAAGAAGCTTATCGAGAGAATGGTCAGGACAGAT 669
           || ||||| || || |||||||||||||| ||||| ||||||| |||||||||| ||
Db     541 CGCGTGACGTCGGACGGCATGCTGTGGAAAAAGCTCATCGAGAGGATGGTCAGGACGGAC 600

Qy     670 TCTCTGTGGAGAGGCCTGGCAGAACGAAGAGGATGGGGACAGTATTTATTCAAAAACAAA 729
           |||||||| |||||||||||||| || ||||| |||||||| || ||||||||||||||||
Db     601 TCTCTGTGGCGAGGCCTGGCAGAGCGCAGAGGCTGGGGACAATACTTATTCAAAAACAAA 660

Qy     730 CCTCCTGACGGGAATGCTCCTCCCAACTCTTTTTATAGAGCACTTTATCCTAAAATTATA 789
           |||||||| | ||| |||||||||||| |||||||||||| |||||||||||||||| |||
Db     661 CCTCCTGATGAGAACGCTCCTCCCAACTCCTTTTATAGAGCGCTTTATCCTAAAATCATA 720

Qy     790 CAAGACATTGAGACAATAGAATCTAATTGGAGATGTGGAAGACATAGTTTACAGAGAATT 849
           |||||||||||||||||||| || |||||||||||||  ||||||||||||||||||||||
Db     721 CAAGACATTGAGACAATAGAGTCCAATTGGAGATGTGGGCGACATAGTTTACAGAGAATC 780

Qy     850 CACTGCCGAAGTGAAACAAGCAAAGGAGTTTACTGTTTACAGTATGATGATCAGAAAATA 909
           |||||||| |||||||||| ||||| ||||||||||||||||| || || ||||| |||
Db     781 CACTGCCGGAGTGAAACAAGTAAAGGGGTTTACTGTTTACAGTACGACGACCAGAAGATA 840

Qy     910 GTAAGCGGCCTTCGAGACAACACAATCAAGATCTGGGATAAAAACACATTGGAATGCAAG 969
           || |||||||||||||||||||| |||||||||||||||||||| |||| ||||||||||
Db     841 GTCAGCGGCCTTCGAGACAACACCATCAAGATCTGGGATAAAAGCACACTGGAATGCAAG 900

Qy     970 CGAATTCTCACAGGCCATACAGGTTCAGTCCTCTGTCTCCAGTATGATGAGAGAGTGATC 1029
           || |||||||| ||||| || || || ||||| ||||| ||||| | |||||| ||||||
Db     901 CGGATTCTCACGGGCCACACGGGCTCCGTCCTGTGTCTGCAGTACGGTGAGAGGGTGATC 960

Qy    1030 ATAACAGGATCATCGGATTCCACGGTCAGAGTGTGGGATGTAAATACAGGTGAAATGCTA 1089
           || ||||| || || || ||||| |||||||||||||||||||||| ||||||| ||||||
Db     961 ATCACAGGCTCCTCAGACTCCACCGTCAGAGTGTGGGATGTAAATGCAGGTGAGATGCTA 1020

Qy    1090 AACACGTTGATTCACCATTGTGAAGCAGTTCTGCACTTGCGTTTCAATAATGGCATGATG 1149
           ||||| |||||||||| |||||||| |||||||| |||| ||||||||||||||||||||
Db    1021 AACACATTGATTCACCACTGTGAAGCCGTTCTGCACCTGCGCTTCAATAATGGCATGATG 1080

Qy    1150 GTGACCTGCTCCAAAGATCGTTCCATTGCTGTATGGGATATGGCCTCCCCAACTGACATT 1209
           |||||||| |||||||| |||||||| ||||| |||||||||| ||||||||||||||||
Db    1081 GTGACCTGTTCCAAAGACCGTTCCATCGCTGTGTGGGATATGGCTTCCCCAACTGACATC 1140

Qy    1210 ACCCTCCGGAGGGTGCTGGTCGGACACCGAGCTGCTGTCAATGTTGTAGACTTTGATGAC 1269
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